

1/32

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Protein and its DNA

<130> 2568W00P

<150> JP 10-323759

<151> 1998-11-13

<150> JP 11-060030

<151> 1999-03-08

<150> JP 11-106812

<151> 1999-04-14

<150> JP 11-166672

<151> 1999-06-14

<150> JP 11-221640

<151> 1999-08-04

<150> JP 11-259818

<151> 1999-09-14

<160> 58

<210> 1

<211> 180

2/32

<212> PRT

<213> Human

<400> 1

Met Glu Ile Ile Ser Ser Lys Leu Phe Ile Leu Leu Thr Leu Ala Thr

1 5 10 15

Ser Ser Leu Leu Thr Ser Asn Ile Phe Cys Ala Asp Glu Leu Val Met

20 25 30

Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg

35 40 45

Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp

50 55 60

Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys

65 70 75 80

Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val

85 90 95

Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser

100 105 110

Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro

115 120 125

Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu

130 135 140

Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu

145 150 155 160

Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln

165 170 175

Lys Gln Ser Arg

180

$\langle 400 \rangle$ 2

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CTAGACCACC TCTATATAAC TGCCCAT

27

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 5

GCACATAGAG ACTTAATTTT AGATTTAGAC

30

<210> 6

<211> 27

<212> DNA

<213> Artificial Sequence

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CATGCACTTT GACTGGTTTC CAGGTAT

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<210> 7

<211> 27

<212> DNA

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CAGCTTTAGG GACAGGCTCC AGGTTTC

27

5/32

<210> 8

<211> 196

<212> PRT

<213> Human

<400> 8

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 Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
 35 40 45
 Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
 50 55 60
 Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
 65 70 75 80
 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
 85 90 95
 Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
 100 105 110
 Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
 115 120 125
 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
 130 135 140
 Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
 145 150 155 160
 Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
 165 170 175

6/32

Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu

180

185

190

Lys Gln Glu Lys

195

<210> 9

<211> 588

<212> DNA

<213> Human

<400> 9

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ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120

TATGACAAAT ATTCTGAGCC TAGAGGATAC CAAAAGGGG AAAGAAGCCT CAATTTTGAG 180

GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240

ATGCCACACT CCTTCGCCAA CTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300

AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCTGGAA GAAATATGGA GGTGAGCCTC 360

GTGAGACGTG TTCCTAACCT GCCCAAAGG TTTGGGAGAA CAACAACAGC CAAAAGTGTC 420

TGCAGGATGC TGAGTGATTT GTGTCAAGGA TCCATGCATT CACCATGTGC CAATGACTTA 480

TTTACTCCA TGACCTGCCA GCACCAAGAA ATCCAGAATC CCGATCAAAA ACAGTCAAGG 540

AGACTGCTAT TCAAGAAAAT AGATGATGCA GAATTGAAAC AAGAAAAA 588

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<223>

<400> 10

GCCTAGAGGA GATCTAGGCT GGGAGGA

27

<210> 11

<211> 27

<212> DNA

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<220>

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<400> 11

GGGAGGAACA TGGAAGAAGA AAGGAGC

27

<210> 12

<211> 27

<212> DNA

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<220>

<223>

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GATGGTGAAT GCATGGACTG CTGGAGC

27

<210> 13

<211> 27

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8/32

<220>

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27

<210> 14

<211> 196

<212> PRT.

<213> Bovine

<400> 14

Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Met Leu Ala Thr
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 20 25 30
 Pro Asn Leu Tyr Ser Lys Lys Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
 35 40 45
 Gly Asp Leu Gly Trp Glu Lys Glu Arg Ser Leu Thr Phe Glu Glu Val
 50 55 60
 Lys Asp Trp Ala Pro Lys Ile Lys Met Asn Lys Pro Val Val Asn Lys
 65 70 75 80
 Met Pro Pro Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Met
 85 90 95
 Glu Glu Glu Arg Ser Thr Arg Ala Met Ala His Leu Pro Leu Arg Leu
 100 105 110
 Gly Lys Asn Arg Glu Asp Ser Leu Ser Arg Trp Val Pro Asn Leu Pro
 115 120 125
 Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Ile Thr Lys Thr Leu
 130 135 140

9/32

Ser Asn Leu Leu Gln Gln Ser Met His Ser Pro Ser Thr Asn Gly Leu
 145 150 155 160
 Leu Tyr Ser Met Ala Cys Gln Pro Gln Glu Ile Gln Asn Pro Gly Gln
 165 170 175
 Lys Asn Leu Arg Arg Arg Gly Phe Gln Lys Ile Asp Asp Ala Glu Leu
 180 185 190
 Lys Gln Glu Lys

195

<210> 15
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 <400> 15
 <210> 15
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<400> 15

ATGGAAATTA TTTCATTAAA ACGATTCATT TTATTGATGT TAGCCACTTC AAGCTTGTTA 60
 ACATCAAACA TCTTCTGCAC AGACGAATCA AGGATGCCCA ATCTTTACAG CAAAAAGAAT 120
 TATGACAAAT ATTCCGAGCC TAGAGGAGAT CTAGGCTGGG AGAAAGAAAG AAGTCTTACT 180
 TTTGAAGAAG TAAAAGATTG GGCTCCAAAA ATTAAGATGA ATAAACCTGT AGTCAACAAA 240
 ATGCCACCTT CTGCAGCCAA CCTGCCACTG AGATTGTTGGA GGAACATGGA AGAAGAAAGG 300

<212> PRT

11/32

<213> Rat

<400> 18

Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr
 1 5 10 15
 Ser Ser Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met
 20 25 30
 Pro His Phe His Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg
 35 40 45
 Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu
 50 55 60
 Lys Asp Trp Gly Ala Lys Lys Asp Ile Lys Met Ser Pro Ala Pro Ala
 65 70 75 80
 Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg
 85 90 95
 Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala
 100 105 110
 Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr
 115 120 125
 Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser
 130 135 140
 Leu His Ser Leu Ala Ser Ser Glu Ser Leu Tyr Ala Met Thr Arg Gln
 145 150 155 160
 His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val
 165 170 175
 Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn
 180 185 190

195

200

<210> 19

<211> 609

<212> DNA

<213> Rat

<400> 19

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TATGGAAAAT	ATTACCAGCT	GAGAGGAATC	CCAAAAGGGG	TAAAGGAAAG	AAGTGTCAC	180
TTTCAAGAAC	TCAAAGATTG	GGGGGCAAAG	AAAGATATTA	AGATGAGTCC	AGCCCCTGCC	240
AACAAAGTGC	CCCACTCAGC	AGCCAACCTT	CCCCTGAGGT	TTGGGAGGAA	CATAGAAGAC	300
AGAAGAAGCC	CCAGGGCACG	GGCCAACATG	GAGGCAGGGA	CCATGAGCCA	TTTTCCCAGC	360
CTGCCCCAAA	GGTTTGGGAG	AACAACAGCC	AGACGCATCA	CCAAGACACT	GGCTGGTTTG	420
CCCCAGAAAT	CCCTGCACTC	CCTGGCCTCC	AGTGAATCGC	TCTATGCCAT	GACCCGCCAG	480
CATCAAGAAA	TTCAGAGTCC	TGGTCAAGAG	CAACCTAGGA	AACGGGTGTT	CACGGAAACA	540
GATGATGCAG	AAAGGAAACA	AGAAAAAATA	GGAAACCTCC	AGCCAGTCCT	TCAAGGGGCT	600
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$\langle 211 \rangle$ 12

<212> DNA

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13/32

12

MGNTTYGGNA AR

<210> 21

<211> 12

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<220>

<223>

<400> 21

12

MGNTTYGGNM GN

<210> 22

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 22

12

MGNWSNGGNA AR

<210> 23

<211> 12

<212> DNA

<213> Artificial Sequence

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<223>

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MGNWSNGGNM GN

<210> 24

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MGNYTNGGNA AR

<210> 25

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<212> DNA

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MGNYTNGGNM GN

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<211> 30

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<210> 27

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25

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16/32

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<212> DNA

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<223>

<400> 31

TTTAGACTTA GACGAAATGG A

21

<210> 32

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 32

GCTCCGTAGC CTCTTGAAGT C

21

<210> 33

<211> 188

<212> PRT

<213> Mouse

<400> 33

17/32

Met Glu Ile Ile Ser Leu Lys Arg Phe Ile Leu Leu Thr Val Ala Thr
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 Ser Ser Phe Leu Thr Ser Asn Thr Phe Cys Thr Asp Glu Phe Met Met
 20 25 30
 Pro His Phe His Ser Lys Glu Gly Asp Gly Lys Tyr Ser Gln Leu Arg
 35 40 45
 Gly Ile Pro Lys Gly Glu Lys Glu Arg Ser Val Ser Phe Gln Glu Leu
 50 55 60
 Lys Asp Trp Gly Ala Lys Asn Val Ile Lys Met Ser Pro Ala Pro Ala
 65 70 75 80
 Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg
 85 90 95
 Thr Ile Asp Glu Lys Arg Ser Pro Ala Ala Arg Val Asn Met Glu Ala
 100 105 110
 Gly Thr Arg Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr
 115 120 125
 Thr Ala Arg Ser Pro Lys Thr Pro Ala Asp Leu Pro Gln Lys Pro Leu
 130 135 140
 His Ser Leu Gly Ser Ser Glu Leu Leu Tyr Val Met Ile Cys Gln His
 145 150 155 160
 Gln Glu Ile Gln Ser Pro Gly Gly Lys Arg Thr Arg Arg Gly Ala Phe
 165 170 175
 Val Glu Thr Asp Asp Ala Glu Arg Lys Pro Glu Lys
 180 185

<210> 34

<211> 564

18/32

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 GACGGAAAAT ACTCCCAGCT GAGAGGAATC CAAAAGGGG AAAAGGAAAG AAGTGTCAGT 180
 TTTCAGAAC TAAAAGATTG GGGGGCAAAG AATGTTATTA AGATGAGTCC AGCCCCTGCC 240
 AACAAAGTGC CCCACTCAGC AGCCAACCTG CCCCTGAGAT TTGGAAGGAC CATAGATGAG 300
 AAAAGAAGCC CCGCAGCAG GGTCAACATG GAGGCAGGGA CCAGGAGCCA TTTCCCCAGC 360
 CTGCCCCAAA GGTTTGGGAG AACAAACAGCC AGAAGCCCCA AGACACCCGC TGATTTGCCA 420
 CAGAAACCCC TGCACTCACT GGGCTCCAGC GAGTTGCTCT ACGTCATGAT CTGCCAGCAC 480
 CAAGAAATTC AGAGTCCTGG TGGAAAGCGA ACGAGGAGAG GAGCGTTTGT GGAAACAGAT 540
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<210> 35

<211> 27

<212> DNA

<213> Artificial Sequence

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<223>

<400> 35

AGTCGACAGT ATGGAGGCGG AGCCCTC

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<210> 36

<211> 29

<212> DNA

<213> Artificial Sequence

19/32

<220>

<223>

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GACTAGTTCA AATGTTCCAG GCCGGGATG

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<210> 37

<211> 432

<212> PRT

<213> Rat

<400> 37

Met Glu Ala Glu Pro Ser Gln Pro Pro Asn Gly Ser Trp Pro Leu Gly

5 10 15

Gln Asn Gly Ser Asp Val Glu Thr Ser Met Ala Thr Ser Leu Thr Phe

20 25 30

Ser Ser Tyr Tyr Gln His Ser Ser Pro Val Ala Ala Met Phe Ile Ala

35 40 45

Ala Tyr Val Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val

50 55 60

Cys Phe Ile Val Leu Lys Asn Arg His Met Arg Thr Val Thr Asn Met

65 70 75 80

Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys

85 90 95

Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp

100 105 110

Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser

115 120 125

Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys

130 135 140

Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Phe

145 150 155 160

Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser

165 170 175

Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Leu Asp

180 185 190

Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro

20/32

195	200	205
Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile		
210	215	220
Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala		
225	230	235
Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala		240
	245	250
Val Ala Glu Gly Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His		255
	260	265
Met Leu Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu		270
	275	280
Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln		285
	290	295
Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala		300
305	310	315
Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu		320
	325	330
Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp		335
	340	345
Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg		350
	355	360
Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly		365
	370	375
Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg		380
385	390	395
Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu		400
	405	410
Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile		415
	420	425
		430

<210> 38

<211> 1299

<212> DNA

<213> Rat

<400> 38

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CCGGTGGCAG CCATGTTTAT CGCGGCCTAC GTGCTCATCT TCCTCCTCTG CATGGTGGGC 180

21/32

AACACCCTGG TCTGCTTCAT TGTGCTCAAG AACCGGCACA TGC GCACTGT CACCAACATG 240
 TTTATCCTCA ACCTGGCCGT CAGCGACCTG CTGGTGGGCA TCTTCTGCAT GCCCACAACC 300
 CTTGTGGACA ACCTTATCAC TGGTTGGCCT TTTGACAACG CCACATGCAA GATGAGCGGC 360
 TTGGTGCAGG GCATGTCCGT GTCTGCATCG GTTTTACAC TGGTGGCCAT CGCTGTGGAA 420
 AGGTTCCGCT GCATCGTGCA CCCTTTCCGC GAGAAGCTGA CCCTTCGGAA GCGCTGTTC 480
 ACCATCGCGG TGATCTGGGC TCTGGCGCTG CTCATCATGT GTCCCTCGGC GGTCACTCTG 540
 ACAGTCACCC GAGAGGAGCA TCACTTCATG CTGGATGCTC GTAACCGCTC CTACCCGCTC 600
 TACTCGTGCT GGGAGGCCTG GCCCGAGAAG GGCATGCGCA AGGTCTACAC CGCGGTGCTC 660
 TTCGCGCACA TCTACCTGGT GCCGCTGGCG CTCATCGTAG TGATGTACGT GCGCATCGCG 720
 CGCAAGCTAT GCCAGGCCCC CGGTCCTGCG CGCGACACGG AGGAGGCGGT GGCCGAGGGT 780
 GGCCGCACTT CGCGCCGTAG GGCCCGCGTG GTGCACATGC TGGTCATGGT GCGCTCTTC 840
 TTCACGTTGT CCTGGCTGCC ACTCTGGGTG CTGCTGCTGC TCATCGACTA TGGGGAGCTG 900
 AGCGAGCTGC AACTGCACCT GCTGTGGTTC TACGCCTTCC CCTTGGCACA CTGGCTGGCC 960
 TTCTTCCACA GCAGCGCCAA CCCCATCATC TACGGCTACT TCAACGAGAA CTTCCGCCGC 1020
 GGCTTCCAGG CTGCCTTCCG TGCACAGCTC TGCTGGCCTC CCTGGGCCGC CCACAAGCAA 1080
 GCCTACTCGG AGCGGCCCAA CCGCCTCCTG CGCAGGCGGG TGGTGGTGGA CGTGCAACCC 1140
 AGCGACTCCG GCCTGCCATC AGAGTCTGGC CCCAGCAGCG GGGTCCCAGG GCCTGGCCGG 1200
 CTGCCACTGC GCAATGGGCG TGTGGCCCAT CAGGATGGCC CGGGGAAGG GCCAGGCTGC 1260
 AACCACATGC CCCTCACCAT CCCGGCCTGG AACATTTGA 1299

<210> 39

<211> 12

<212> PRT

<213> Artificial Sequence

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<223> the C-terminus of the polypeptide is amide (-CONH₂) form

22/32

<400> 39

Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe
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<210> 40

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> the C-terminus of the polypeptide is amide (-CONH₂) form

<400> 40

Val Pro Asn Leu Pro Gln Arg Phe

1 5

<210> 41

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> the C-terminus of the polypeptide is amide (-CONH₂) form

<400> 41

Ser Ala Gly Ala Thr Ala Asn Leu Pro Arg Ser

1 5 10

<210> 42

<211> 36

<212> DNA

<213> Human

<400> 42

23/32

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36

<210> 43

<211> 36

<212> DNA

<213> Human

<400> 43

AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCT

36

<210> 44

<211> 24

<212> DNA

<213> Human

<400> 44

GTTCTAACC TGCCCCAAAG GTTT

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<210> 45

<211> 276

<212> DNA

<213> Human

<400> 45

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ACATCAAACA TTTTGTGTC AGATGAATTA GTGATGTCCA ATCTTCACAG CAAAGAAAAT 120

TATGACAAAT ATTCTGAGCC TAGAGGATAC CAAAAGGGG AAAGAAGCCT CAATTTTGAG 180

GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240

ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTT 276

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<211> 336

<212> DNA

<213> Human

24/32

<400> 46

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 TATGACAAAT ATTCTGAGCC TAGAGGATAC CCAAAGGGG AAAGAAGCCT CAATTTTGAG 180
 GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240
 ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300
 AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCT 336

<210> 47

<211> 393

<212> DNA

<213> Human

<400> 47

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 TATGACAAAT ATTCTGAGCC TAGAGGATAC CCAAAGGGG AAAGAAGCCT CAATTTTGAG 180
 GAATTAAAAG ATTGGGGACC AAAAAATGTT ATTAAGATGA GTACACCTGC AGTCAATAAA 240
 ATGCCACACT CCTTCGCCAA CTTGCCATTG AGATTTGGGA GGAACGTTCA AGAAGAAAGA 300
 AGTGCTGGAG CAACAGCCAA CCTGCCTCTG AGATCTGGA AGAAATATGGA GGTGAGCCTC 360
 GTGAGACGTG TTCCTAACCT GCCCCAAAGG TTT 393

<210> 48

<211> 27

<212> DNA

<213> Artificial Sequence

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<400> 48

25/32

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<223>

<400> 49

AGCGATTCAT TTTATTGACT TTAGCA

26

<210> 50

<211> 203

<212> PRT

<213> Rat

<400> 50

Met Glu Ile Ile Ser Ser Lys Arg Phe Ile Leu Leu Thr Leu Ala Thr

1 5 10 15

Ser Ser Phe Leu Thr Ser Asn Thr Leu Cys Ser Asp Glu Leu Met Met

20 25 30

Pro His Phe His Ser Lys Glu Gly Tyr Gly Lys Tyr Tyr Gln Leu Arg

35 40 45

Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu

50 55 60

Lys Asp Trp Gly Ala Lys Lys Asp Ile Lys Met Ser Pro Ala Pro Ala

65 70 75 80

Asn Lys Val Pro His Ser Ala Ala Asn Leu Pro Leu Arg Phe Gly Arg

26/32

	85	90	95
Asn Ile Glu Asp Arg Arg Ser Pro Arg Ala Arg Ala Asn Met Glu Ala			
100	105	110	
Gly Thr Met Ser His Phe Pro Ser Leu Pro Gln Arg Phe Gly Arg Thr			
115	120	125	
Thr Ala Arg Arg Ile Thr Lys Thr Leu Ala Gly Leu Pro Gln Lys Ser			
130	135	140	
Leu His Ser Leu Ala Ser Ser Glu Leu Leu Tyr Ala Met Thr Arg Gln			
145	150	155	160
His Gln Glu Ile Gln Ser Pro Gly Gln Glu Gln Pro Arg Lys Arg Val			
165	170	175	
Phe Thr Glu Thr Asp Asp Ala Glu Arg Lys Gln Glu Lys Ile Gly Asn			
180	185	190	
Leu Gln Pro Val Leu Gln Gly Ala Met Lys Leu			
195	200		

<210> 51

<211> 609

<212> DNA

<213> Rat

<400> 51

ATGGAAATTA TTTCATCAAA GCGATTCATT TTATTGACTT TAGCAACTTC AAGCTTCTTA	60
ACTTCAAACA CCCTTTGTTC AGATGAATTA ATGATGCCCC ATTTTCACAG CAAAGAAGGT	120
TATGGAAAAT ATTACCAGCT GAGAGGAATC CCAAAAGGGG TAAAGGAAAG AAGTGTCAC	180
TTTCAAGAAC TCAAAGATTG GGGGGCAAAG AAAGATATTA AGATGAGTCC AGCCCCTGCC	240
AACAAAGTGC CCCACTCAGC AGCCAACCTT CCCCTGAGGT TTGGGAGGAA CATAGAAGAC	300

27/32

AGAAGAAGCC CCAGGGCACG GGCCAACATG GAGGCAGGGA CCATGAGCCA TTTTCCCAGC 360
 CTGCCCCAAA GGT TTGGGAG AACACAGCC AGACGCATCA CCAAGACACT GGCTGGTTTG 420
 CCCCAGAAAT CCCTGCACTC CCTGGCCTCC AGTGAATTGC TCTATGCCAT GACCCGCCAG 480
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Ser Ser Tyr Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val

35 40 45

Ala Tyr Ala Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val

50 55 60

Cys Phe Ile Val Leu Lys Asn Arg His Met His Thr Val Thr Asn Met

65 70 75 80

Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys

85 90 95

Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp

100 105 110

Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser

115 120 125

Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys

130 135 140

Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Val

145 150 155 160

Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser

165 170 175

Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Val Asp

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Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro

29/32

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Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe Ser His Ile		
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Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Pro Gly Gly Glu Glu Ala		240
245	250	255
Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val His Met Leu		
260	265	270
Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu Trp Ala		
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Leu Leu Leu Leu Ile Asp Tyr Gly Gln Leu Ser Ala Pro Gln Leu His		
290	295	300
Leu Val Thr Val Tyr Ala Phe Pro Phe Ala His Trp Leu Ala Phe Phe		
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Asn Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu Asn Phe		320
325	330	335
Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Arg Leu Cys Pro Arg Pro		
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Ser Gly Ser His Lys Glu Ala Tyr Ser Glu Arg Pro Gly Gly Leu Leu		
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His Arg Arg Val Phe Val Val Val Arg Pro Ser Asp Ser Gly Leu Pro		
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Ser Glu Ser Gly Pro Ser Ser Gly Ala Pro Arg Pro Gly Arg Leu Pro		
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Leu Arg Asn Gly Arg Val Ala His His Gly Leu Pro Arg Glu Gly Pro		400
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 AACACCCTGG TCTGTTTCAT CGTGCTCAAG AACCGGCACA TGCATACTGT CACCAACATG 240
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 CGCAAGCTCT GCCAGGCCCC GGGCCCGGCC CCCGGGGGCG AGGAGGCTGC GGACCCGCGA 780
 GCATCGCGGC GCAGAGCGCG CGTGGTGCAC ATGCTGGTCA TGGTGGCGCT GTTCTTCACG 840
 CTGTCCTGGC TGCCGCTCTG GCGGCTGCTG CTGCTCATCG ACTACGGGCA GCTCAGCGCG 900
 CCGCAGCTGC ACCTGGTCAC CGTCTACGCC TTCCCCTTCG CGCACTGGCT GGCCTTCTTC 960
 AACAGCAGCG CCAACCCCAT CATCTACGGC TACTTCAACG AGAACTTCCG CCGCGGCTTC 1020
 CAGGCCGCCCT TCCGCGCCCC CCTCTGCCCC CGCCCGTCGG GGAGCCACAA GGAGGCCTAC 1080
 TCCGAGCGGC CCGGCGGGCT TCTGCACAGG CGGGTCTTCG TGGTGGTGCG GCCCAGCGAC 1140
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31/32

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 CCTGTGGCGG CCATGTTTCAT TGTGGCCTAT GCGCTCATCT TCCTGCTCTG CATGGTGGGC 180
 AACACCCTGG TCTGTTTCAT CGTGCTCAAG AACC GG CACA TGCATACTGT CACCAACATG 240
 TTCATCCTCA ACCTGGCTGT CAGTGACCTG CTGGTGGGCA TCTTCTGCAT GCCCACCACC 300
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KIKUCHI, KUNIKO
TERAO, YASUKO
SHINTANI, YASUSHI
HINUMA, SHUJI
FUKUSUMI, SHOJI
FUJII, RYO
HOSOYA, MASAKI
KITADA, CHIEKO

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1				5					10					15					
tca	agc	ttg	tta	aca	tca	aac	att	ttt	tgt	gca	gat	gaa	tta	gtg	atg				96
Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Ala	Asp	Glu	Leu	Val	Met				
			20					25					30						
tcc	aat	ctt	cac	agc	aaa	gaa	aat	tat	gac	aaa	tat	tct	gag	cct	aga				144
Ser	Asn	Leu	His	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg				
		35					40					45							
gga	tac	cca	aaa	ggg	gaa	aga	agc	ctc	aat	ttt	gag	gaa	tta	aaa	gat				192
Gly	Tyr	Pro	Lys	Gly	Glu	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp				
	50					55					60								
tgg	gga	cca	aaa	aat	gtt	att	aag	atg	agt	aca	cct	gca	gtc	aat	aaa				240
Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys				
65					70					75					80				

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85 90 95	
caa gaa gaa aga agt gct gga gca aca gcc aac ctg cct ctg aga tct	336
Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser	
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gga aga aat atg gag gtg agc ctc gtg aga cgt gtt cct aac ctg ccc	384
Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro	
115 120 125	
caa agg ttt ggg aga aca aca aca gcc aaa agt gtc tgc agg atg ctg	432
Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu	
130 135 140	
agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta	480
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu	
145 150 155 160	
ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa	528
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		20						25					30		

Ser	Asn	Leu	His	Ser	Lys	Glu	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg
	35						40					45			

Gly	Tyr	Pro	Lys	Gly	Glu	Arg	Ser	Leu	Asn	Phe	Glu	Glu	Leu	Lys	Asp
	50					55					60				

Trp	Gly	Pro	Lys	Asn	Val	Ile	Lys	Met	Ser	Thr	Pro	Ala	Val	Asn	Lys
65					70					75				80	

Met	Pro	His	Ser	Phe	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Val
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Gln	Glu	Glu	Arg	Ser	Ala	Gly	Ala	Thr	Ala	Asn	Leu	Pro	Leu	Arg	Ser
			100					105					110		

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Gln Arg Phe Gly Arg Thr Thr Thr Ala Lys Ser Val Cys Arg Met Leu
130 135 140

agt gat ttg tgt caa gga tcc atg cat tca cca tgt gcc aat gac tta 480
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
145 150 155 160

ttt tac tcc atg acc tgc cag cac caa gaa atc cag aat ccc gat caa 528
Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
165 170 175

aaa cag tca agg aga ctg cta ttc aag aaa ata gat gat gca gaa ttg 576
Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
180 185 190

aaa caa gaa aaa taa 591
Lys Gln Glu Lys
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			20					25					30				
Pro	Asn	Leu	Tyr	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg		
		35					40					45					
Gly	Asp	Leu	Gly	Trp	Glu	Lys	Glu	Arg	Ser	Leu	Thr	Phe	Glu	Glu	Val		
	50					55					60						
Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys	Met	Asn	Lys	Pro	Val	Val	Asn	Lys		
65					70					75					80		
Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Met		
				85					90					95			
Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu	Pro	Leu	Arg	Leu		
			100					105					110				
Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn	Leu	Pro		
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Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu		
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Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu		
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Leu	Tyr	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln		
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1				5				10						15			
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Ser	Ser	Leu	Leu	Thr	Ser	Asn	Ile	Phe	Cys	Thr	Asp	Glu	Ser	Arg	Met		
		20						25						30			
ccc	aat	ctt	tac	agc	aaa	aag	aat	tat	gac	aaa	tat	tcc	gag	cct	aga	144	
Pro	Asn	Leu	Tyr	Ser	Lys	Lys	Asn	Tyr	Asp	Lys	Tyr	Ser	Glu	Pro	Arg		
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50						55						60					
aaa	gat	tgg	gct	cca	aaa	att	aag	atg	aat	aaa	cct	gta	gtc	aac	aaa	240	
Lys	Asp	Trp	Ala	Pro	Lys	Ile	Lys	Met	Asn	Lys	Pro	Val	Val	Asn	Lys		
65				70						75				80			
atg	cca	cct	tct	gca	gcc	aac	ctg	cca	ctg	aga	ttt	ggg	agg	aac	atg	288	
Met	Pro	Pro	Ser	Ala	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	Asn	Met		
				85				90						95			
gaa	gaa	gaa	agg	agc	act	agg	gcg	atg	gcc	cac	ctg	cct	ctg	aga	ctc	336	
Glu	Glu	Glu	Arg	Ser	Thr	Arg	Ala	Met	Ala	His	Leu	Pro	Leu	Arg	Leu		
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Gly	Lys	Asn	Arg	Glu	Asp	Ser	Leu	Ser	Arg	Trp	Val	Pro	Asn	Leu	Pro		
		115				120						125					
cag	agg	ttt	gga	aga	aca	aca	aca	gcc	aaa	agc	att	acc	aag	acc	ctg	432	
Gln	Arg	Phe	Gly	Arg	Thr	Thr	Thr	Ala	Lys	Ser	Ile	Thr	Lys	Thr	Leu		
130						135						140					
agt	aat	ttg	ctc	cag	cag	tcc	atg	cat	tca	cca	tct	acc	aat	ggg	cta	480	
Ser	Asn	Leu	Leu	Gln	Gln	Ser	Met	His	Ser	Pro	Ser	Thr	Asn	Gly	Leu		
145				150						155				160			
ctc	tac	tcc	atg	gcc	tgc	cag	ccc	caa	gaa	atc	cag	aat	cct	ggg	caa	528	
Leu	Tyr	Ser	Met	Ala	Cys	Gln	Pro	Gln	Glu	Ile	Gln	Asn	Pro	Gly	Gln		
				165				170						175			

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35 40 45

Gly Ile Pro Lys Gly Val Lys Glu Arg Ser Val Thr Phe Gln Glu Leu
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85 90 95

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1		5				10					15					
																96
tca	agc	ttc	tta	act	tca	aac	acc	ctt	tgt	tca	gat	gaa	tta	atg	atg	
Ser	Ser	Phe	Leu	Thr	Ser	Asn	Thr	Leu	Cys	Ser	Asp	Glu	Leu	Met	Met	
			20		25					30						
																144
ccc	cat	ttt	cac	agc	aaa	gaa	ggg	tat	gga	aaa	tat	tac	cag	ctg	aga	
Pro	His	Phe	His	Ser	Lys	Glu	Gly	Tyr	Gly	Lys	Tyr	Tyr	Gln	Leu	Arg	
			35		40					45						
																192
gga	atc	cca	aaa	ggg	gta	aag	gaa	aga	agt	gtc	act	ttt	caa	gaa	ctc	
Gly	Ile	Pro	Lys	Gly	Val	Lys	Glu	Arg	Ser	Val	Thr	Phe	Gln	Glu	Leu	
50		55					60									
																240
aaa	gat	tgg	ggg	gca	aag	aaa	gat	att	aag	atg	agt	cca	gcc	cct	gcc	
Lys	Asp	Trp	Gly	Ala	Lys	Lys	Asp	Ile	Lys	Met	Ser	Pro	Ala	Pro	Ala	
65		70					75					80				
																288
aac	aaa	gtg	ccc	cac	tca	gca	gcc	aac	ctt	ccc	ctg	agg	ttt	ggg	agg	
Asn	Lys	Val	Pro	His	Ser	Ala	Ala	Asn	Leu	Pro	Leu	Arg	Phe	Gly	Arg	
				85		90					95					

aac	ata	gaa	gac	aga	aga	agc	ccc	agg	gca	cgg	gcc	aac	atg	gag	gca	336
Asn	Ile	Glu	Asp	Arg	Arg	Ser	Pro	Arg	Ala	Arg	Ala	Asn	Met	Glu	Ala	
			100						105				110			
ggg	acc	atg	agc	cat	ttt	ccc	agc	ctg	ccc	caa	agg	ttt	ggg	aga	aca	384
Gly	Thr	Met	Ser	His	Phe	Pro	Ser	Leu	Pro	Gln	Arg	Phe	Gly	Arg	Thr	
			115					120				125				
aca	gcc	aga	cgc	atc	acc	aag	aca	ctg	gct	ggg	ttg	ccc	cag	aaa	tcc	432
Thr	Ala	Arg	Arg	Ile	Thr	Lys	Thr	Leu	Ala	Gly	Leu	Pro	Gln	Lys	Ser	
			130				135					140				
ctg	cac	tcc	ctg	gcc	tcc	agt	gaa	tcg	ctc	tat	gcc	atg	acc	cgc	cag	480
Leu	His	Ser	Leu	Ala	Ser	Ser	Glu	Ser	Leu	Tyr	Ala	Met	Thr	Arg	Gln	
						150				155					160	
cat	caa	gaa	att	cag	agt	cct	ggg	caa	gag	caa	cct	agg	aaa	cgg	gtg	528
His	Gln	Glu	Ile	Gln	Ser	Pro	Gly	Gln	Glu	Gln	Pro	Arg	Lys	Arg	Val	
				165					170					175		
ttc	acg	gaa	aca	gat	gat	gca	gaa	agg	aaa	caa	gaa	aaa	ata	gga	aac	576
Phe	Thr	Glu	Thr	Asp	Asp	Ala	Glu	Arg	Lys	Gln	Glu	Lys	Ile	Gly	Asn	
				180				185					190			
ctc	cag	cca	gtc	ctt	caa	ggg	gct	atg	aag	ctg	tga					612
Leu	Gln	Pro	Val	Leu	Gln	Gly	Ala	Met	Lys	Leu						
			195				200									

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<210> 20
<211> 12
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Probe
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<220>  
<221> modified_base  
<222> (9)  
<223> a, c, t, g, other or unknown
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<400> 20
mgnttyggna ar

12

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<210> 21
<211> 12
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Probe

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<223> a, c, t, g, other or unknown
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<220>
 <221> modified_base
 <222> (9)
 <223> a, c, t, g, other or unknown

<220>
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 <222> (12)
 <223> a, c, t, g, other or unknown

<400> 21
 mgnttyggnm gn

12

<210> 22
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<220>
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 <223> a, c, t, g, other or unknown

<220>
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<220>
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 <223> a, c, t, g, other or unknown

<400> 22
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12

<210> 23
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<220>
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 <222> (3)
 <223> a, c, t, g, other or unknown

<220>
 <221> modified_base

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Ser Gln Leu Arg Gly Ile Pro Lys Gly Glu Lys Glu Arg Ser Val Ser
45 50 55 60

<400> 36
gactagttca aatgttccag gccgggatg

aaccacatgc ccctcaccat cccggcctgg aacatttga

1299

<210> 39
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 39
 Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe
 1 5 10

<210> 40
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 40
 Val Pro Asn Leu Pro Gln Arg Phe
 1 5

<210> 41
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 41
 Ser Ala Gly Ala Thr Ala Asn Leu Pro Arg Ser
 1 5 10

<210> 42
 <211> 36
 <212> DNA
 <213> Homo sapiens

<400> 42
 atgccacact ccttcgccaa cttgccattg agattt

36

<210> 43
 <211> 36
 <212> DNA
 <213> Homo sapiens

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<210> 48
<211> 27
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<210> 54
<211> 430
<212> PRT
<213> Homo sapiens
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<400> 54

Met Glu Gly Glu Pro Ser Gln Pro Pro Asn Ser Ser Trp Pro Leu Ser
1 5 10 15

Gln Asn Gly Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe
20 25 30

Ser Ser Tyr Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val
35 40 45

Ala Tyr Ala Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val
50 55 60

Cys Phe Ile Val Leu Lys Asn Arg His Met His Thr Val Thr Asn Met
65 70 75 80

Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys
85 90 95

Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp
100 105 110

Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser
115 120 125

Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys
130 135 140

Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Val
145 150 155 160

Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser
165 170 175

Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Val Asp
180 185 190

Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro
195 200 205

Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe Ser His Ile
210 215 220

Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala Arg Ile Ala
225 230 235 240

Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Pro Gly Gly Glu Glu Ala
245 250 255

Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val His Met Leu
260 265 270

Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu Trp Ala
275 280 285

Leu Leu Leu Leu Ile Asp Tyr Gly Gln Leu Ser Ala Pro Gln Leu His
290 295 300

Leu Val Thr Val Tyr Ala Phe Pro Phe Ala His Trp Leu Ala Phe Phe
305 310 315 320

Asn Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu Asn Phe
325 330 335

Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Arg Leu Cys Pro Arg Pro
340 345 350

Ser Gly Ser His Lys Glu Ala Tyr Ser Glu Arg Pro Gly Gly Leu Leu
355 360 365

His Arg Arg Val Phe Val Val Val Arg Pro Ser Asp Ser Gly Leu Pro
370 375 380

Ser Glu Ser Gly Pro Ser Ser Gly Ala Pro Arg Pro Gly Arg Leu Pro
385 390 395 400

Leu Arg Asn Gly Arg Val Ala His His Gly Leu Pro Arg Glu Gly Pro
405 410 415

Gly Cys Ser His Leu Pro Leu Thr Ile Pro Ala Trp Asp Ile
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<210> 55
<211> 1290
<212> DNA
<213> Homo sapiens

<400> 55
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cctgtggcgg ccatgttcat tgtggcctat gcgctcatct tctgtcttg catggtgggc 180
aacacctgg tctgtttcat cgtgtcaag aaccggcaca tgcatactgt caccaacatg 240
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cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
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aggttccgct gcatcgtgca ccttttccgc gagaagctga ccctgcggaa ggcgctcgtc 480
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ctgcggaatg ggcggtggc tcaccacggc ttgcccaggg aagggcctgg ctgctcccac 1260
ctgcccctca ccattccagc ctgggatata 1290

<210> 56
<211> 1290

<212> DNA

<213> Homo sapiens

<400> 56

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cctgtggcgg ccattgttcat tgtggcctat gcgtcatct tctgtctctg catggtgggc 180
aacacctggt tctgtttcat cgtgctcaag aaccggcaca tgcatactgt caccaacatg 240
ttcatcctca acctggctgt cagtgcctg ctgggtgggca tcttctgcat gccaccacc 300
cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
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ctgcggaatg ggcgggtggc tcaccacggc ttgccaggg aagggcctgg ctgctccac 1260
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<210> 57

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

31

<400> 57

gtcgacatgg agggggagcc ctcccagct c

<210> 58

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

29

<400> 58

actagttcag atatcccagg ctggaatgg

<210> 59

<211> 4

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 59
Phe Met Arg Phe
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<210> 60
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 60
Leu Pro Leu Arg Phe
1 5

<210> 61
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 61
Leu Pro Leu Arg Ser
1 5

<210> 62
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 62
Leu Pro Gln Arg Phe
1 5

<210> 63
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 63

Leu Pro Leu Arg Leu
1 5